



TOP PAGE | QUERY | RESULTS | PROJECTS | VIEWS | DATABANKS

HELP

View ☐ * Complete entries * ☒This entry is from: DDBJRELEASE:AE008898DDBJRELEASESaveLinkLaunchNCIstallWPrinter Friendly

LOCUS AE008898 23880 bp DNA linear BCT 31-JUL-2002

DEFINITION *Salmonella typhimurium* LT2, section 202 of 220 of the complete genome.

ACCESSION AE008898 AE006468

VERSION AE008898.1

KEYWORDS

SOURCE *Salmonella typhimurium* LT2

ORGANISM *Salmonella typhimurium* LT2

Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; *Salmonella*.

REFERENCE 1 (bases 1 to 23880)

AUTHORS McClelland, M., Sanderson, K. E., Spieth, J., Clifton, S. W., Latreille, P., Courtney, L., Porwollik, S., Ali, J., Dante, M., Du, F., Hou, S., Layman, D., Leonard, S., Nguyen, C., Scott, K., Holmes, A., Grewal, N., Mulvaney, E., Ryan, E., Sun, H., Florea, L., Miller, W., Stoneking, T., Nhan, M., Waterston, R. and Wilson, R. K.

TITLE Complete genome sequence of *Salmonella enterica* serovar Typhimurium LT2

JOURNAL Nature 413 (6858), 852-856 (2001)

MEDLINE 21534948

PUBMED 11677609

REFERENCE 2 (bases 1 to 23880)

AUTHORS The *Salmonella typhimurium* Genome Sequencing Project.

TITLE Direct Submission

JOURNAL Submitted (29-MAR-2001) Genome Sequencing Center, Department of Genetics, Washington University School of Medicine, 4444 Forest Park Boulevard, St. Louis, MO 63108, USA

COMMENT COMMENT Supported by NIH grant 5U 01 AI43283

Coding sequences below are predicted from manually evaluated computer analysis, using similarity information and the programs; GLIMMER; <http://www.tigr.org/softlab/glimmer/glimmer.html> and GeneMark; <http://opal.biology.gatech.edu/GeneMark/>

EC numbers were kindly provided by Junko Yabuzaki and the Kyoto Encyclopedia of Genes and Genomes; <http://www.genome.ad.jp/kegg/>, and Pedro Romero and Peter Karp at EcoCyc; <http://ecocyc.PangeaSystems.com/ecocyc/>

The analyses of ribosome binding sites and promoter binding sites were kindly provided by Heladia Salgado, Julio Collado-Vides and ReguonDB; http://kinich.cifn.unam.mx:8850/db/regulondb_intro.frameset

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistries or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one m13 subclone.

FEATURES

source Location/Qualifiers

1..23880

/organism="Salmonella typhimurium LT2"

/strain="LT2; SGSC 1412; ATCC 700720"

/db_xref="ATCC:700720"

/db_xref="taxon:99287"

/note="LT2"

gene 107..1036

/gene="malM"

/note="synonym: STM4232"

RBS 107..112

/gene="malM"
 /note="putative RBS for malM; RegulonDB:STMS1H004137"
 119..1036
 /gene="malM"
 /note="maltose operon periplasmic protein precursor.
 (SW:MALM_SALTY)"
 /codon_start=1
 /transl_table=11
 /product="periplasmic protein of mal regulon"
 /protein_id="AAL23056.1"
 /db_xref="GI:16422790"
 /translation="MKMKKSLVALCLTAGLFASVPGISLAENVYVPQNTSAAPVIPAA
 ALQQLTWTPVDQSKTQSTQLATGGQRLDVAGITGPVAAYSVPANIGELTLTLTSEVVK
 QASVFAPNVILLDQNMTPSAFFPSSYFTYQQPGVMSADRLEGVMRLTPALGQKLYVL
 VFTTEKDLQQTTLTLDPAKAYAKGVGNSIPDIPDPVARHTTDGVVKLVKNTSSSSVL
 VGPLFGSSSGTPVTVGNTAAPVAAPAPVAPKSEPMLNDTESYFNKA1KDAVAKGDVD
 KALKLLDEAERLGSTSARSTFISSVKGKG"
 1203..1714
 /gene="ubiC"
 /note="synonym: STM4233"
 1203..1208
 /gene="ubiC"
 /note="putative RBS for ubiC; RegulonDB:STMS1H004138"
 1217..1714
 /gene="ubiC"
 /EC_number="4.-.-"
 /note="similar to E. coli chorismate lyase (AAC77009.1);
 Blastp hit to AAC77009.1 (202 aa), 86% identity in aa 38 -
 202"
 /codon_start=1
 /transl_table=11
 /product="chorismate pyruvate lyase"
 /protein_id="AAL23057.1"
 /db_xref="GI:16422791"
 /translation="MSHPALTQLRALRYFDAIPALEPHLLDWLLEDSTMRFEQGGK
 RVSVTLIREFVQGSEVEEASGLLPSESRYWLREILLCADGEPWLAGRTVVPSTLCG
 PEQVLQHLGKTPLGRYLFSTLTRDFIEIGRDATLWGRSRLRLSGKPLLLTELFLP
 ASPLY"
 1715..2600
 /gene="ubiA"
 /note="synonym: STM4234"
 1715..1720
 /gene="ubiA"
 /note="putative RBS for ubiA; RegulonDB:STMS1H004139"
 1728..2600
 /gene="ubiA"
 /EC_number="2.5.1."
 /note="similar to E. coli
 4-hydroxybenzoate-octaprenyltransferase (AAC77010.1);
 Blastp hit to AAC77010.1 (290 aa), 93% identity in aa 1 -
 290"
 /codon_start=1
 /transl_table=11
 /product="p-hydroxybenzoate: octaprenyltransferase"
 /protein_id="AAL23058.1"
 /db_xref="GI:16422792"
 /translation="MEWSLTQSKLLAFHRLMRTDKPIGALLLLWPTLWALWVATPGMP
 QLWILAVFVAGVWLMRAAGCVVNDYADRFKFDGHVKRTVNRPLPSGAVTEKEARNLFVV
 LVLLAFLVLTLNAMTILLVAALALAWVYPMKRYTHLPQVVLGAAGFWSIPMAFAA
 VSESLPLSCWLMFLANILWAVAYDTQYAMVDRDDDIKIGIKSTAILFGRYDTLIIIGIL
 QLGVMALMALIGWLNGLGWGYWAVLVAGALFVYQKLIANREREACFAFMNNNNYVG
 LVFLGLAMSYWHF"
 complement(2699..5136)
 /gene="plsB"
 /note="synonym: STM4235"
 complement(2699..5119)
 /gene="plsB"
 /EC_number="2.3.1.15"
 /note="similar to E. coli glycerol-3-phosphate
 acyltransferase (AAC77011.1); Blastp hit to AAC77011.1
 (827 aa), 94% identity in aa 21 - 826"

```

/codon_start=1
/transl_table=11
/product="glycerolphosphate acyltransferase activity"
/protein_id="AAL23059.1"
/db_xref="GI:16422793"
/translation="MSGWPRIYYKLLNPLSLVKSKSIPAEPAGELGDTSRPIMYV
LPYNSKADLLTLRAQCLAHDLDPLEPLEIDGALLPRYVFHGGPRVFTYYPKEESV
KLFHDYLDLHRSNPALDVQMPVSVMFGRAPGREKGEDNPPLRLNGVQKFFAISWLG
RDSFVRFSPSVSLRRMADEHGTDKIIAQKLARVARMHFAQRQLAAVGPRLPARQDLFN
KLLASKAIARAVEDEARSKKISHEKAQNAIALMEEIAANFSYEMIRLTDRLGFTWN
RLYQGIVHNAERVRLAHDGHEIVYVPCRSHMDYLLLSYVLVYHQLVPPHIAAGIN
LNFWPAGPIFRRLGAFFIRRTFKGNKLYSTVFREYLGELFSRGYSVEYFVEGGRSRTG
RLDPKTGTLSTMIQAMLRGGTRPITLVPIYIGYEHVMEVGTYAKELRGATKEKESLP
QMLKGLSKLRNLGGQYVNFGEPMPLMTYLNQHVPEWRESIDPIEAIAPAWLTPTVNSI
AADLMVRINNAGANAMNLCCTALLASRQSLTREQLTEQLDCYLDLMRNPYSTDST
VPAASAGELIAHALQMNKFEVEKDTIGDIIILPREQAVLMTYYRNNIAHMLIMPSLMA
AIIITQHRRISRDALQQHVEALYPMLKAELFLRWEREELASVIDALASEMQRQGLITLQ
DDELHINPTHSRTLQLLAAGARETLQRYAITFWLLSANPSINRSTLEKESRTVAQRLS
VLHGINAPEFFDKAVFSSVLTLRDEGYISDTGDAEPAETMKIYQMLADLITSDVRLT
IESATQGE"
RBS complement(5131..5136)
/gene="plsB"
/Note="putative RBS for plsB; RegulonDB:STMS1H004140"
gene 5278..5658
/gene="dgkA"
/Note="synonym: STM4236"
RBS 5278..5283
/gene="dgkA"
/Note="putative RBS for dgkA; RegulonDB:STMS1H004141"
CDS 5290..5658
/gene="dgkA"
/EC_number="2.7.1.107"
/Note="similar to E. coli diacylglycerol kinase
(AAC77012.1); Blastp hit to AAC77012.1 (122 aa), 86%
identity in aa 1 - 121"
/codon_start=1
/transl_table=11
/product="diacylglycerol kinase"
/protein_id="AAL23060.1"
/db_xref="GI:16422794"
/translation="MANNTTGFTRIIKAAGYSWKGFRAAWTHEAAFRQESLAVLLGVI
IACWLDVDAITRVLLIGSVLLIMIVEILNSAIEAVVDRIQSEYHELSGRAKDMGSAAV
LLSIFVALMTWGILLWSHFR"
gene 5701..6375
/gene="lexA"
/Note="synonym: STM4237"
-35_signal 5701..5709
/gene="lexA"
/Note="putative -35_signal for lexA;
RegulonDB:STMLTH004657"
protein_bind 5722..5738
/gene="lexA"
/Note="putative binding site for LexA, RegulonDB:
STMS1H000241"
/bound_moiety="LexA"
-10_signal 5725..5733
/gene="lexA"
/Note="putative -10_signal for lexA;
RegulonDB:STMLTH004657"
protein_bind 5742..5762
/gene="lexA"
/Note="putative binding site for LexA, RegulonDB:
STMS1H000249"
/bound_moiety="LexA"
RBS 5756..5761
/gene="lexA"
/Note="putative RBS for lexA; RegulonDB:STMS1H004142"
CDS 5767..6375
/gene="lexA"
/EC_number="3.4.21.88"
/Note="transcriptional repressor (LexA family); LEXA

```

```

repressor. (SW:LEXA_SALTY)"
/codon_start=1
/transl_table=11
/product="SOS response regulator"
/protein_id="AAL23061.1"
/db_xref="GI:16422795"
/translation="MKALTARQQEVFDLIRDHISQTGMPPTRAEIAQRLGFRSPNAEE
EHLKALARKGVLEIVSGASRGIRLLQEEEDGLPLVGRVAAGEPLLAQQHIEGHYQVDP
SLFKPSADFLRVSGMSMKDIGMDGDLAVHKTQDVRNGQVVVARIDDEVTVKRLKK
QGNKVPELLPENSEFTPIVVDLREQSFTIEGLAVGVIRNGEWL"
gene 6540..7878
      /gene="dinF"
      /note="synonym: STM4238"
RBS 6540..6545
      /gene="dinF"
      /note="putative RBS for dinF; RegulonDB:STMS1H004143"
CDS 6553..7878
      /gene="dinF"
      /note="induced by UV and mitomycin C; SOS, lexA regulon;
similar to E. coli DNA-damage-inducible protein F
(AAC77014.1); Blastp hit to AAC77014.1 (459 aa), 89%
identity in aa 19 - 457"
      /codon_start=1
      /transl_table=11
      /product="DNA-damage-inducible protein F"
      /protein_id="AAL23062.1"
      /db_xref="GI:16422796"
      /translation="MPLFTSSDKALWRLALPMIFSNIIVPLLGLVDTAVIGHLDSPVF
LGGVAVGATATSFLLMLLLFLRMSTTGLTAQAFGAKNPQALARALIQLLLALGAGVM
IVLFRTPLIELALHIVGGNDAVLVQARRFLEIRWLSAPASLANLVLLGWLLGVQYARA
PVILLVGNILNIALDLWLVMGLHMNVQGAALATVIAEYVTLILGLMMVRKVLHLRGV
SLDMLKQAWRGNVRRLLALNRDILRLSLLLQLCFGAITVSGARLGSIIAVNAVLMTL
LTFTAYALDGFAYAVEAHSGQAYGARDGSKLLDVWRAACRQSGIALLFSTVYALAGE
HIVALLTSLPQIQLLADRYLIWQVVLPLVGVWCYLLDGMFI GATRAAEMRNSMAVAAG
GFALTFLFALPVLGNHGLWLALT VFLALRGLSLSLI WRRHWREGTWFAFS"
gene 7875..7988
      /gene="STM4239"
CDS 7875..7988
      /gene="STM4239"
      /note="hypothetical protein"
      /codon_start=1
      /transl_table=11
      /product="putative cytoplasmic protein"
      /protein_id="AAL23063.1"
      /db_xref="GI:16422797"
      /translation="MTVKNSEYKTEGRIPAYNYHVQKQLQSIWANNTCYS"
gene 7998..8219
      /gene="yjbJ"
      /note="synonym: STM4240"
RBS 7998..8003
      /gene="yjbJ"
      /note="putative RBS for yjbJ; RegulonDB:STMS1H004144"
CDS 8007..8219
      /gene="yjbJ"
      /note="similar to E. coli orf, hypothetical protein
(AAC77015.1); Blastp hit to AAC77015.1 (69 aa), 95%
identity in aa 1 - 69"
      /codon_start=1
      /transl_table=11
      /product="putative cytoplasmic protein"
      /protein_id="AAL23064.1"
      /db_xref="GI:16422798"
      /translation="MMNKDEAGGNWKQFKGKMKEQWGKLTDDDMTVIEGKRDQLVGKI
QERYGYQKDQAEKEVVDWETRNNYRW"
gene complement(8318..8843)
      /gene="zur"
      /note="synonym: STM4241"
CDS complement(8318..8833)
      /gene="zur"
      /note="Fur family; similar to E. coli putative regulator
(AAC77016.1); Blastp hit to AAC77016.1 (191 aa), 92%"

```

identity in aa 21 - 191"
/codon_start=1
/transl_table=11
/product="transcriptional repressor of znuABC operon"
/protein_id="AAL23065.1"
/db_xref="GI:16422799"
/translation="MEKTTTQELLAQAEKLCARQNVRLTPQRLEVLRLMSLQQGAISA
YOLLDLLRETEPQAKPPTIYRALDFLEQGFVHKVESTNSYVVCFLFDQPTHSSAMFI
CDRCGVVKEECAEGVEDIMHTLAAKMGFALRHNVIEAHGLCPACVEVEACRHPGNCGH
DHSVLVKKKPR"
RBS complement(8838..8843)
/gene="zur"
/note="putative RBS for zur; RegulonDB:STMS1H004145"
gene 9076..10390
/gene="STM4242"
RBS 9076..9081
/gene="STM4242"
/note="putative RBS for STM4242; RegulonDB:STMS1H004146"
CDS 9080..10390
/gene="STM4242"
/codon_start=1
/transl_table=11
/product="putative outer membrane or exported protein"
/protein_id="AAL23066.1"
/db_xref="GI:16422800"
/translation="MNKNVKLSLIAIAVSLFMAKQASAANTWEARN DAMGGTGVASA
NYGSGVLLNPALLAKAKPEDNITVVLPAVGVI TDKNLQDEIDDISKVDYDEVVD
NLTGLQILLNPRGVNLNQFQGAARDLADELEYLNGKTARANAGAGLAVSIPGQTLVAF
IAKGYAHGRVSSSIDQNDIQYLRDIQHDervalREAGRAALLGSDEITKHLNSTASGR
VAIVSDYGI ALAKQFVVGVPVSI GVTPLKQKTWLYNYTTSIYNYDSSDWNSSRYRND
DTGFNIDAGLAADI GENWTLGVSGQNLVSRDIDTKDIYITNGMTGETTNYKDTYQIRP
LVTAGIAWHNDLLTVSADGDLTETKGFKSEDNSQYVGVGAEVRPLSWLAVRAGYRADV
KNNDNSNVVTGGLGFAPFNRVHLDLMGLYGEDETWGAGAQLTMTF"
gene 10478..11476
/gene="yjbN"
/note="synonym: STM4243"
CDS 10478..11476
/gene="yjbN"
/note="possibly dehydrogenases; nifR3 family; similar to
E. coli orf, hypothetical protein (AAC77019.1); Blastp hit
to AAC77019.1 (345 aa), 90% identity in aa 7 - 345"
/codon_start=1
/transl_table=11
/product="putative TIM-barrel enzyme"
/protein_id="AAL23067.1"
/db_xref="GI:16422801"
/translation="MQPETQSSALPAYRFSIAPMLDWTDRHCYFLRLLSRQTQLYTE
MVTTGAI IHGKGDYLAISEEEHPVALQLGGSDPAQLAHCAKLAARGYDEINLNVGCP
SDRVQNGMFGACLMGNAQLVADCVKAMRDVVSIPVTVKTRIGIDDQDSYAFLCDFIDT
VSGQGECEMFI IHARKAWLSGLSPKENREIPPLDYPRVYQLKRDPHLTMSINGGKS
LEEAKEHLRHMDGMVVGREAYQNP GILAAVDREIFGADTTDADPVAVVRAMYPIERE
LSQGAYLGHITRHLGLFQGI PGARQWRRYLSNAHKAGADVAVLEQALKLVADKR"
gene 11631..11886
/gene="yjbO"
/note="synonym: STM4244"
RBS 11631..11636
/gene="yjbO"
/note="putative RBS for yjbO; RegulonDB:STMS1H004147"
CDS 11644..11886
/gene="yjbO"
/note="similar to E. coli orf, hypothetical protein
(AAC77020.1); Blastp hit to AAC77020.1 (150 aa), 82%
identity in aa 71 - 150"
/codon_start=1
/transl_table=11
/product="putative inner membrane protein"
/protein_id="AAL23068.1"
/db_xref="GI:16422802"
/translation="MLELLFVLGFFLMLMVTGVSLGILAAVLVATAVMFLGGMFALM
IKLLPWLLAVAVVWVIKAVKTPKIPQYQRNNRRFY"
gene complement(12061..13052)

CDS /gene="qor"
/note="synonym: STM4245"
complement(12061..13044)
/gene="qor"
/EC_number="1.6.5.5"
/note="similar to E. coli quinone oxidoreductase
(AAC77021.1); Blastp hit to AAC77021.1 (327 aa), 90%
identity in aa 1 - 327"
/codon_start=1
/transl_table=11
/product="NADPH dependent quinone oxidoreductase"
/protein_id="AAL23069.1"
/db_xref="GI:16422803"
/translation="MATRIEFHKKHGGPEVLQTVEFTPAPAEHEIQVENKAIIGINFID
TYIRSGLYPPPSLPAGLGTEAAGVVSKVGNVGEHIVRGDRVVYAQSTLGAYSSVHNVT
ADKAAIILPDAISFEQAAASFLKGLTVFYLLRKYEVKPDPEFLHAAAGGVGLIACQW
AKALGAKLIGTVGSAQKAQRALDAGAWQVINYREESI VERVEITGGKKVRVVYDSVG
KDTWEASLDCLQRRGLMVSFGNASGPVTGVNLGILNQKGSLYATRPSLQGYITTREEL
TEASNELFSLIASGVIKVDVAENQRYALKDARRAHEVLESRATQGSLLIP"
RBS complement(13047..13052)
/gene="qor"
/note="putative RBS for qor; RegulonDB:STMS1H004148"
gene 13091..14524
/gene="dnaB"
/note="synonym: STM4246"
RBS 13091..13096
/gene="dnaB"
/note="putative RBS for dnaB; RegulonDB:STMS1H004149"
CDS 13109..14524
/gene="dnaB"
/EC_number="3.6.1.-"
/note="chromosome replication; chain elongation;
replicative DNA helicase. (SW:DNAB_SALTY)"
/codon_start=1
/transl_table=11
/product="putative replicative DNA helicase"
/protein_id="AAL23070.1"
/db_xref="GI:16422804"
/translation="MAGNKPFPNKPTDARDPQVAGIKVPPHSIEAEQSVLGGLMLD
NERWDDVAERVVAEDFYTRPHRHIFTEMGRLESGSPIDLITLAESLERQGQLDSVGG
FAYLAELSKNTPSAANI SAYADIVREAVVRDMIAVAHEIADAGYDPQGRNSDELLDL
AESRVFQIAENRANKDEGPKSIDQILDATVARIQLFQQPHDGVTVGDTGYQDLNKKT
AGLQRSDLIIVAARPSMGKTTFAMNLCENAAMLQDKPVLIFSLEMPGEQIMMRMLASL
SRVDQTRIRTGQLDDEDDWARISGTMGILLEKRNMYIDSSGLTPTEVRSRARRIFREH
GGLSLIMIDYQLMRVPSLSDNRTLEIAEISRLKALAKELQVPVVALSQLNRSLEQR
ADKRPVNSDLRESGIEQDADLIMFIYRDEVYHENSCLKGIAEIIIGKQRNGPIGTVR
LTFNGQWSRFDNYAGPQYDDE"
gene 14545..15635
/gene="alr"
/note="synonym: STM4247"
RBS 14545..14550
/gene="alr"
/note="putative RBS for alr; RegulonDB:STMS1H004150"
CDS 14556..15635
/gene="alr"
/EC_number="5.1.1.1"
/note="alanine racemase, biosynthetic. (SW:ALR1_SALTY)"
/codon_start=1
/transl_table=11
/product="biosynthetic alanine racemase 1"
/protein_id="AAL23071.1"
/db_xref="GI:16422805"
/translation="MQAATVVINRRALRHNLRQLRELAPASKLVAVVKANAYGHGLLE
TARTLPDADFQVARLEEALRLRAGGITQPIILLLEGFFDAADLPTISAQCLHTAVHNQ
EQLAALEAVELAEPTVVMKLDGTGMHRLGVRPEEAFAFYQLRTHCKNVQRPVNI VSHF
ARADEPECGATEHQLDIFNAFCQKPGQRSIAASGGILLWPQSHFDWARPGIILYGVS
PLEHKPWGPDFGFQPVMSLTSSLI AVRDKHAGEPVGYGGTWWVSERDTRLGVVAMGYGD
GYPRAAPSGTPVLVNGREVPVIGVRVAMDMI CVDLGPNAQDNAGDPVVLWGEGLPVERI
AEMTKVSAYELITRLTSRVAMKYID"
gene 15773..17014
/gene="tyrB"

/note="synonym: STM4248"
 -35_signal 15773..15781
 /gene="tyrB"
 /note="putative -35_signal for tyrB;
 RegulonDB:STMLTH004658"
 protein_bind 15794..15816
 /gene="tyrB"
 /note="putative binding site for TyrR, RegulonDB:
 STMS1H000389"
 /bound_moiety="TyrR"
 -10_signal 15800..15808
 /gene="tyrB"
 /note="putative -10_signal for tyrB;
 RegulonDB:STMLTH004658"
 RBS 15806..15811
 /gene="tyrB"
 /note="putative RBS for tyrB; RegulonDB:STMS1H004151"
 protein_bind 15820..15844
 /gene="tyrB"
 /note="putative binding site for TyrR, RegulonDB:
 STMS1H000384"
 /bound_moiety="TyrR"
 CDS 15821..17014
 /gene="tyrB"
 /EC_number="2.6.1.57"
 /note="tyrosine repressible; aromatic-amino-acid
 aminotransferase. (SW:TYRB_SALTY)"
 /codon_start=1
 /transl_table=11
 /product="tyrosine aminotransferase"
 /protein_id="AAL23072.1"
 /db_xref="GI:16422806"
 /translation="MFQKVDAYAGDPILSLMERFKDDSRHDKVNLSIGLYNEDGIIP
 QLKTVAEAEARLNAQPHGASLYLPMEGLNTYRHTIAPLLFGADHPVLQQQRVATIQT
 GGSGALKVGADEFKRYFPDAGVWVSDPTWENHIAIFAGAGFEVSTYPWYDDATNGIRF
 NDLLATLNTLPARSIVLLHPCCHNPTGADLTPSQWDAVIEIVKARDLIPFLDIAYQGF
 GAGMDDDAYVIRAIASAGLPALVSNFSKIFSLYGERVGGLSVVCDEAIEARVLGQL
 KATVRRYISSPPCFGAQVVATVLGDEALKAGWLAEVDAMRNRNIIISMRQTLVKELKAEM
 PDRNFDYLLQQRGMFSYTGLSEEQVDRLRDEFGVYLIIASGRMCVAGLNASNVHRVAKA
 FAAVM"
 gene 17190..17914
 /gene="aphA"
 /note="synonym: STM4249"
 RBS 17190..17195
 /gene="aphA"
 /note="putative RBS for aphA; RegulonDB:STMS1H004152"
 CDS 17201..17914
 /gene="aphA"
 /EC_number="3.1.3.2"
 /note="similar to E. coli diadenosine tetraphosphatase
 (AAC77025.1); Blastp hit to AAC77025.1 (237 aa), 89%
 identity in aa 1 - 237"
 /codon_start=1
 /transl_table=11
 /product="non-specific acid
 phosphatase/phosphotransferase, class B"
 /protein_id="AAL23073.1"
 /db_xref="GI:16422807"
 /translation="MKKITLALSAVCLLFTLNHSANALVSSPSTLNPGTNVAKLAEEA
 PVHWVVAQIENSLTGRPPMAVGFDIDDTVLFSSPGFWRGKKTYSPODDYLKNPAFW
 EKMNGWDEFSIPKEVARQLIDMHVRRGDSIYFVTGRSQTKTETVSKTLADNFHII
 PAA NMNPVIFAGDKPEQNTKVQWLQEKNMRIIFYGDSNDNITAARDGIRGIRILRAANSTY
 KPLPQAGAFGEVIVNSEY"
 gene 18031..18459
 /gene="yjbQ"
 /note="synonym: STM4250"
 RBS 18031..18036
 /gene="yjbQ"
 /note="putative RBS for yjbQ; RegulonDB:STMS1H004153"
 CDS 18043..18459
 /gene="yjbQ"

```

/feature="note" /note="similar to E. coli orf, hypothetical protein
(AAC77026.1); Blastp hit to AAC77026.1 (138 aa), 78%
identity in aa 1 - 138"
/codon_start=1
/transl_table=11
/product="putative cytoplasmic protein"
/protein_id="AAL23074.1"
/db_xref="GI:16422808"
/translation="MWYQRTITLSEKPRGFHLITDEITDKLSGLPPVETGLLHLLLLH
TSASLTLENCDPTVRADMERHFLKTPDNAAYEHYEGADDMPSHIKSSVLGVSLLL
PVRQGRLLQLGTWQGIWLGEHRIHGGPRKIIATLQGE"
gene 18449..18818
/feature="gene" /gene="yjbR"
/feature="note" /note="synonym: STM4251"
RBS 18449..18454
/feature="RBS" /gene="yjbR"
/feature="note" /note="putative RBS for yjbR; RegulonDB:STMS1H004154"
CDS 18462..18818
/feature="CDS" /gene="yjbR"
/feature="note" /note="similar to E. coli orf, hypothetical protein
(AAC77027.1); Blastp hit to AAC77027.1 (118 aa), 92%
identity in aa 1 - 117"
/codon_start=1
/transl_table=11
/product="putative cytoplasmic protein"
/protein_id="AAL23075.1"
/db_xref="GI:16422809"
/translation="MTISELLQYCMAPGAEQSVHSDWKATQIKVEDVLFAMVKEVEG
RPAASLKTSPLEALLRQQHSDVRPSRHLNKAHWSTVYLDGSLPDSQLYYLVDASYQQ
AVNALSEDKRKQLPQS"
gene complement(18819..19163)
/feature="gene" /gene="STM4252"
CDS complement(18819..19157)
/feature="CDS" /gene="STM4252"
/codon_start=1
/transl_table=11
/product="putative inner membrane protein"
/protein_id="AAL23076.1"
/db_xref="GI:16422810"
/translation="MASINEIHYLITTAQAEHPVASSAIAEFIQTYKQARESDDAIR
ESAAFIARALQEHARGWLDLDDMIILLEGQRDLARLRANNAQIALGSRIRSTVIRLID
IALALLVGAL"
gene complement(19144..19602)
/feature="gene" /gene="STM4253"
CDS complement(19144..19599)
/feature="CDS" /gene="STM4253"
/codon_start=1
/transl_table=11
/product="putative outer membrane lipoprotein"
/protein_id="AAL23077.1"
/db_xref="GI:16422811"
/translation="MENTMKLPYAITLLLCLFLSACTLPDRFSAYAFQQLTLLQARST
RFLQDAARIPWQKETLLKDDRDIRQIFFQAERVARQGGDKHRLDNLALLKNHYLRLYA
RVMRRKQPLTYIQAERYQQNNQYWKLAIQGECLHWGARCTQGDENG VY"
RBS complement(19158..19163)
/feature="RBS" /gene="STM4252"
/feature="note" /note="putative RBS for STM4252; RegulonDB:STMS1H004155"
RBS complement(19597..19602)
/feature="RBS" /gene="STM4253"
/feature="note" /note="putative RBS for STM4253; RegulonDB:STMS1H004156"
gene complement(19731..22719)
/feature="gene" /gene="uvrA"
/feature="note" /note="synonym: STM4254"
CDS complement(19731..22556)
/feature="CDS" /gene="uvrA"
/feature="note" /note="complexes with UvrBC; excinuclease ABC subunit A.
(SW:UVRA_SALTY)"
/codon_start=1
/transl_table=11
/product="DNA excision repair enzyme"
/protein_id="AAL23078.1"

```



```

/db_xref="GI:16422812"
/translation="MDKIEVRGARTHNLKNINLVIPRDKLIVVTGLSGSGKSSLAFTD
LYAEGQRRYVESLSAYARQFLSLMEKPOVDHIEGLSPAISIEQKSTSHNPRSTVGTIT
EIHDLRLLLFARVGEPRCPDHDVPLAAQTVSQMDNVL SQPEGKRLMLLAPIKERKG
EHTKTLENLASQGYIRARIDGEVCDLSDPPKLELQKKHTIEVVIDRFKVRNDLSQRLA
ESFETALELSGGTAVVADMDEKAEELFSANFACPICGYSMRELEPRLFSFNNPAGA
CPTCDGLGVQQYFDPDRVIQNPDLSLAGAI RGWDRRNFFYFQMLKSLAEHYKFDVDA
PWASLSANVHKVVL YGSGKENIEFKYMNDRGDTSVRRHPFEGVLHNMERRYKETESSA
VREELAKFI SNRPCASCEGTRLNREARHVFVENTPLPAISDMSIGHAMDDFTNLKLSG
QRAKIAEKVLKEIGDRLKFLVNVGLNYLTLSRSAETLSGGEAQRIRLASQIGAGLVGV
MYVLDEPSIGLHQRDNERLLGTLIHLRNLGNTVIVVEHDEDAIRAADHVIDIGPGAGV
HGGEVVAEGPLEAIMAVPESLTGQYMSGKRKIEVPKQRVPANPEKVLKLTGARGNNLK
DVTLTLPVGLFTCTIGVSGSGKSTLINDTLFPIAQRQLNGATIAEPAPYRDIQGLEHF
DKVIDIDQSPIGRTPRSNPATYTGVTVPVRELFAGVPESRSRGYTPGRFSFNVRRGRC
EACQGDGVIKVMHFLPDIYVPCDQCKGKRYNRETLEIKYKGKTIHEVLDMTIEEARE
FFDAVPALARKLQTLMDVGLTYIRLGQSATTL SGGEAQRVKLARELSKRGTGQTLIIL
DEPTTGLHFADIQQLDVLHQLRDQGNTIVVIEHNLVDVIKTADWIVDLGPEGSGSGGGE
ILVAGTPETVAEASHTARFLKPMLK"

gene      22521..22637
/ gene="STM4255"
CDS       22521..22637
/ gene="STM4255"
/ codon_start=1
/ transl_table=11
/ product="putative cytoplasmic protein"
/ protein_id="AAL23079.1"
/ db_xref="GI:16422813"
/ translation="MGAGAPNFDLIHSPFPVETRMPLFEGQTAETANYDTI"
RBS       complement(22558..22563)
/ gene="uvrA"
/ note="putative RBS for uvrA; RegulonDB:STMS1H004157"
protein_bind 22638..22658
/ note="putative binding site for LexA, RegulonDB:
STMS1H000246"
/ bound_moiety="LexA"
protein_bind complement(22638..22656)
/ gene="uvrA"
/ note="putative binding site for LexA, RegulonDB:
STMS1H000244"
/ bound_moiety="LexA"
-10_signal complement(22695..22703)
/ gene="uvrA"
/ note="putative -10_signal for uvrA;
RegulonDB:STMLTH004659"
gene      22704..23334
/ gene="ssb"
/ note="synonym: STM4256"
-35_signal 22704..22712
/ gene="ssb"
/ note="putative -35_signal for ssb;
RegulonDB:STMLTH004660"
-35_signal complement(22711..22719)
/ gene="uvrA"
/ note="putative -35_signal for uvrA;
RegulonDB:STMLTH004659"
-10_signal 22731..22739
/ gene="ssb"
/ note="putative -10_signal for ssb;
RegulonDB:STMLTH004660"
RBS       22790..22795
/ gene="ssb"
/ note="putative RBS for ssb; RegulonDB:STMS1H004158"
CDS       22804..23334
/ gene="ssb"
/ note="controls activity of RecBCD nuclease; single-strand
binding protein (SSB) (helix-destabilizing protein).
(SW:SSB_SALTY)"
/ codon_start=1
/ transl_table=11
/ product="ssDNA-binding protein"
/ protein_id="AAL23080.1"

```

/db_xref="GI:16422814"

/translation="MASRGVNKVLVGNLGGDPEVRYMPSGGAVANLTATSESWRDK
QTGEMKEQTEWHRVVMFGKLAEVAGEYLRKGSQVYIEGQLRTRKWTQSGGQERYTTEI
NVPQIGGYMQLGGRRGGGAPAGGQQGGWGPQQPQQGNGQFSGGAQSRPQQSAP
APSNEPPMDFDDIPF"BASE COUNT 5356 a 6155 c 6630 g 5739 t
ORIGIN

```
1 catcaggtct gatgatgctt gtaagccgaa taaggcgcca gccgccattc ggcatatgt
61 ttgggttggc gcgctattgc ctggctaccg ctgaacccgc cttattgagg tgagaataat
121 gaaaatgaag aaaagtctcg tcgcccctcg tttaaccgca gggctgticg ccagcgtgcc
181 gggatatcagc ctggcggaag tgaactatgt accgcaaaat accagcgccg cggccgttat
241 tcctgtctgt gcgctacagc aattaacctg gacgcctgta gatcagltca aaacgcagtc
301 tacccaactg gcgactggcg gccagcgctt tgacgtcgcc ggcatlaccg gcccggtcgc
361 cgcttatagc gttccggcga atatcggcga gctgacatta actctgacca ccgaggtcaa
421 taagcaagcc agcgtttttg cgccaaacgt gtgatictt gaccaaata tgacgccttc
481 ggctttcttc cccagcagtt actttactta tcagcagccg ggctgatga gcgcagaccg
541 gctgggaaggc gtgatggccc tgacgcctgt gttggggcag cagaaactct atgttctggt
601 gtttacgacc gaaaaagatc ttacgcaaac cactacgctg ctcgatccgg caaaagccta
661 tgccaaaggc gtcggttaact ctatcccggg tattcccgat ccagttgctc gccataccac
721 tgacggcgtg gtgaaactga aggtgaaaac caacagcagc tccagcgatg tggtcgggcc
781 gtgttttggc tcgtccggta ccggcccggt aacggtaggc aataccggcg cggcggtcgc
841 tgcgccagcg ccagtcgcgc cgaagaaaaa cgagccgatg ttgaacgata cggaaagcta
901 ctttaataaa gcgattaaag atcccgtagc gaaagccgac gtcgataaag ccgtgaaact
961 gcttgatgag gccgaacgtc tgggatcgac atctgcccgt tccaccttta tcagcaggtt
1021 aaaaggcaag gggtaatat ttccccacag tgcgtatgtt gcagcaactg gtgcgtctcc
1081 tggcgccact ttttttatca ttcatgcga attgttattt tttgttggc caacagatca
1141 cttaatgtg attggcccc ccgtaatgtc tttctgaga tacaatgact ttaggttatg
1201 aatcgagag taaggcatgt cacaccctgc gttaacgcaa ctgcgtgcgc tgcgctattt
1261 tgatgcgatt cctgcgcttg aacccccatt gctggactgg ctgttgcctg aagattctat
1321 gactaaacgt ttgagcagc agggaaaagc ggttaagcgt acgctgattc gggaaagcgtt
1381 tgcggccaa agtgaggctg aggaagcact aggtttactg ccatccgagt cccgctacig
1441 gttacgtgag atactgcttt gcgctgacgg cgagccctgg ctgcccggac gtaccgtggt
1501 accggaatcc acgctgtgcg gacctgaaca ggtcttacia catctgggta aaacccccgt
1561 tggacgttat ctatttacct catcgacact gaccgcgat tttattgaaa ttggacgcga
1621 tgcaacgcgt tggggcgccc gctctcgact gcggttgagc ggaanaaccgc tgttgcctac
1681 cgagcttttt ttacctgcat cgccgctgta ctgagaggaa gataaagatg gattggagtc
1741 tgacgcagag taagctgctg gcgtttcacc gtttgatgct tacagataag cctattggcg
1801 cgctgctgct gctctggccc acgctttggg cgctatgggt ggcgaccccg ggtatgcctc
1861 agctgtggat ttggcgagt ttgtcgctg gcgtgtgggt aatgcgcgcg gcggcgctcg
1921 tggtaaaatg ttatgccgat cgtaaatttg acggacatgt aaaacgtacg gtcaaccggc
1981 ctttaccag cggcgccgtg acagagaaaag aagcgcgcaa ccgtttgtg ttgctgtgtc
2041 tgcctggcgt tctgttgggt ctgacgctga acgcatgac gattctgctt tccgtggcgg
2101 cgctggcgtt ggccctgggt tatcccttta tgaacgcga caccacactg ccgcaggtcg
2161 tgcctggggc cgctttcgcc tggtaaatcc ccatggcggt cggccgggtg agcgaatccc
2221 tgcggttgag ctgctggctg atgttctcgt ccaatattct ctgggcagtg gcttacgata
2281 cgcaatatgc gatgctgac agagatgatg atatcaagat aggcattaaa tcaacggcga
2341 tcttgtttgg tcgttatgac acattgatta tcgggattct gcagcttggc gtcatggcgt
2401 taatggcgct gatcgctgg ttgaatggct tgggatgggg atattactgg gctgtgctgg
2461 tggcgggcgc gctgtttgtc taccagcaaa aactgattgc gaaccgtgag cgtgaagcct
2521 gctttaaagc ctttatgaac aataactacg ttggcctggt gctattttta gggctggcga
2581 tgagttactg gcacttctga tgcataggcg ggccgacccg gccataaag ccaaaatttt
2641 caatacgtca tatcagttgc ccgataagct tacgccatcg ggcatctcag gcactggctt
2701 actcgccctg cgtcgcgctt tcaatcgtca gacggacatc agaggtaatc agatcggcga
2761 gcatctgata tatcttctac gtttctcgcc gttcggcatc gcccgtaica ctgataaac
2821 cctcatccc tagcgtaac acgagtgaac tgaacaccgc ttgtcgaaa aactccggcg
2881 cgtttaatac gtcaggaca gacagacgtt gcgccacggt acggctttct ttctccagcg
2941 tactggcgtt gatggacgga ttggcgctca acagccagaa cgtaatggca taacgtctga
3001 gcggtttcgc cgcccgctgc gccagcagtt gcagcgtagc ggaatgcgtc gggttgatat
3061 gcagttcatc atcctgcagg gtaattagcc cctgacgctg catttactg gccagcgctt
3121 caatgaccga ggttaactcc tcgcctccc agcgaggaa cagctccgtt ttaacatcg
3181 gatagagcgc ttcaaatgac tgcgtcaacg catcacgca aatgcgacga tgcgtgggtg
3241 taatcgccgc catcagcgaa ggcataatca acatatgcgc gatattgtta cgtatgtagg
3301 tcatcaaac acgctgctcg cgccggcaga tgatgatatc gccaatgggt tctttctcga
3361 cctcaaacct attcatctgc agcgctgag cgataagctc gccagcgctg cggcgaggaa
3421 cggttgagtc tgtggaataa gggacattgc gcatcagatc gagatagcaa tcaagctgct
3481 cggtagcgtc ctgcgggtg agcgagcgtt gacgcgacgc taacagcgcg gtacaacaca
3541 ggttcatcgc gtttgcgcgc ccagcgttgt taatacgcac catcagatcg gcggcgatc
3601 tatttaccgt cggcgtagc cagcgtaggc gtatggcctc tatagggtcg atagattcgc
3661 gccactccgg cacatgctgg ttcaggtagc tcatgagcgg catcggttcg ccaaagttaa
3721 cgtagccctg acccagattg cgcagcttgc tcaagccttt cagcatctcg ggacgctct
3781 ctttctcttt tgcgcggcg cgagttctt tcgcataggt gccacttcc atgacgtgct
```

3841 catagccgat gtaaataggg actaacgtaa ttggacgggt accgccgcgc agcatcgcc
3901 ggatagtcac cgacagggtg ccggttttcg ggtctaacaa acgtccggta cgcgaacgtc
3961 ctctttcgac aaaatactca accgagtaac cgcggctgaa cagttcggcc aggtattcgc
4021 gaaagacggg ggaatagagt ttattccctt taaaggctgc acgaataaag aacgcgccca
4081 gacgacggaa aatcggggcca gcgggccaga aattaagggtt aataccggcg gcaatgtgcg
4141 gcggaaccag tccctgggtg tacagcacat aagaaaggag caagtagtcc atatggctgc
4201 ggtgacaggg tacatagacg atttcatgcc cgtcgtgcgc cagttggcgt acgcgtcgcg
4261 cgttatgcac gttaatcccc tggtaaagtc ggttcagggt aaaccccaaa atccgtcgcg
4321 tcaaacgaat catctcgtaa gagaagttcg ccgcgatctc ttccatcagc gcaatggcgt
4381 ttgtcgtcgc tttttcatga gagatttttt tactgcgcgc ttgcgtctct accgcgcggg
4441 cgatcgcttt cgaggccagc agtttggtta acagatcctg acggcgaggc aggcgtgggc
4501 caaccgcgcg caggcgctgg cgagcaaagt gcatacgcgc caccggagcc agcttctgcg
4561 cgaatgattt atcgggtccg tgitcatcag ccatacgacg caatgagacg gacggcgaga
4621 atcggacaaa gctatcgca cccagccagg agatggcaaa gaatttctgt accgcgttca
4681 gcatacgtaa aggcgggtta tcttctccct ttacacgacc cggcgcgcgc ccaaacatca
4741 cggaaacggg caccatctgc acgtccaaag ccggaattact ccgatgcaga tccgagataat
4801 cgtgaaaaag ttaccacgac tcttcttttg cgtgtaata ggtaaagaca cgcggtccgc
4861 cgtgaataaa tacatagcgt ggcaacagcg cgcggtcgtat ctccagcggtat tccagcggtat
4921 ccgggagatc gtgcgcgaga caatgcgcgc gcagcgtcag taagtcgcgt tttagattgt
4981 atggcaagac atacataatg gggcgagaag tatcgagccc caattctcgg cggggttccg
5041 ccggaataga ctgtcttttt accagtatgc ttaattggtaa attcagtaat tttagtataa
5101 ttctgggcca gccggacata aacgatgtaa agcctctggt taataatgca aatgcggtgc
5161 aaggatatca gaaagttag cgaatttctg ttgtatcccc tcatcttcg cgttcggtta
5221 cggcagtcgc aatcgtgcag ggcaaccgta taatgtcatt gacgttaata atgtaaaaag
5281 gttcttttga tggccaataa taccactgga ttaccagaa ttatcaaaag ggcaggatat
5341 tcttggaag gatttcgcgc cgcatggact caggaagcgg cgttcgccca ggaagacctc
5401 cgggtattgc tggcgctcat catcgctcgc tggctggatg tggatgcgat taccgtgtg
5461 ttattgatag gttccgtttt acttatcatg attgtgaaa tcttcaacag cgtattgaa
5521 gcggtcgtgg accgcacatc tctgaatac catgagcttt ccggccgtgc gaaagatatg
5581 ggatcggctg cgggtcctat gttctatttc gttgccctga tgacctgggg catctgttta
5641 tggtcacatt ttcgataaag gttccaaatt ttataaatct ctgtttttt gcgccgtttg
5701 tggttccaaa atcaccttta actgtatata ctacacgat gatgtatat acaccagggg
5761 ggccggaatga aagcgttaac ggccaggcaa caagagggtg ttgatctcat cgggatacac
5821 atcagccaga caggatgcc accgacgcgt gcggaatcg cgcagcgttt ggggttccgt
5881 tccccaaacg cggcgggaag acaccttaaa gcgctggcgc gcaaaagggt gcttgaatc
5941 gtttcggcgc catcgcgagg tatcgtctg ttacaggaag aagaggacgg attaccgctt
6001 gtccggcgctg tccggcgccc tgaaccgctt ctggcgagc agcatattga agccattac
6061 caggtcgac cttcgtgtt caaaccagc gccgatttc tgcgtcgcgt gagcggtatg
6121 tcatgaaag acatcggtat tatggtggg gatttgctgg cgttacataa aacgcaggac
6181 gtccgtaatg gccagggtgt tgcgtcgc attgatgatg aagtgcagat aaaacgcctg
6241 aaaaagcagg gcaataaagt gagctcgtc ccggaataa cgcagtttac accgatagtg
6301 gtggatctgc gcgaacaaag cttacgatt gaaggcctgg cgttaggcgt cttcgcaac
6361 ggggaatggt ttagtctct ttttaatctc ctgttaagcc gccatccggc aatcgtgtag
6421 ctgatggcg ctgcgttat caggcctacg ggaatgcagt tcttgagatg attaatgtgt
6481 aggcgggata aggcgttacg tgcacatccg caatgcgctc gtttcgttta actcctgtc
6541 aggcctttct ccatgcgctt tttaccctc tctgataaag cttcttgcgc tcttgcgttg
6601 ccgatgattt tttctaacat caccgtcccc ttactggggc tggtcgatac ggcgggtatt
6661 ggtcatctgg acagccctgt tttctgggc ggcgtggcgg tggcgcgac tgcaccagc
6721 tttcttttca tgcgtcgtt atttctacgt atgagacca ccggcctaac ggcgcaggca
6781 ttggcgcca aaaaaccgca ggcgttagcc cggcgctca ttcaaccgtt attgtggcg
6841 ctggcgcgag cgttgatgat tgtctattt cgcacgcgcg ttatcgagct ggccttatat
6901 atgtcggcg ggaacgacgc tgtcttggtg caggcgagac gcttcttga aattcgttgg
6961 ctaagcgtc ccgcgtcact ggcaaatctg gtgctgctcg gttggctgtt aggcgttcag
7021 taigcggcg cgccggttat ctgttggtg tggggcaata tcttcaata cgcgtcgc
7081 ctgtggctgg tgaagggtt tcatatgaac gtgcagggtg ctgccctggc agcggtcatc
7141 gcagaatatg taccgttact gatcgccctc atgatggtag gtaaaagtct ccatctccgc
7201 ggtgtgtcgc tggatatgtt aaaacaggcc tggcgcgcca acgtgcgcgc cttttggcg
7261 ctcaatcgcg atatcatgt gcgctcattg ctccctcagc ttgtttttg cgcaatcacg
7321 gtgtcaggcg cgcggctggg cagcgatat ttcgcggtta atgcagctct gatgacctta
7381 ctcaccttta cggcctatgc gctggacggt ttgtcttatg cgttggaggc gcactccggt
7441 caggcttacg gcgcgcgtga cgttagcaag ctactggagc tctggcgagc ggcgtgtcgt
7501 cagtcaggaa ttgtggcctt gttgttttcc acagcttatg ccttggcagg cgaacataat
7561 gtcgctttac tgacctatt gccgcaata cagctactgg cggatcggtta tcttatctgg
7621 cagggtggtat taccgctggt ggcggtatgg tctatctgc tgcagggtat gtttatggc
7681 gcgacgcgcg ctggcgaat gcgcaatagc atggcagtcg ccgcgggagg attcgcgtg
7741 acgctcttcg ccttgccggt attaggaaat catggtttat ggcctggcatt aaccgtgttc
7801 ctggcgcttc gcggtctgtc gttgagcctt atctggcgtc gtcactggcg cgagggtaca
7861 tggtttgcca gatcgtgacg gttaaaaatt ctgaatataa aaccgaaggc cgaattcctg
7921 cctacaatta ttatcacgct cagcagaaat tgcagagcat ttggcggaat aacacctgct
7981 attcctaacc gaatgatgag gacaagatga tgaataaaga cgaagccgcg gtaacttga
8041 aacagtittaa aggtaaaatg aaagaacaaat ggggcaaaact gaccgatgac gatatgacgc

8101 ttatcgaagg taaacgcgac caactggtag gtaaaatcca ggagcggttac ggttaccaga
8161 aagatcaggc ggaaaaagag gtgttgact gggaaacccg taacaactat cgctggtaat
8221 atgttttccc ctaccaggag tacatggatg tgcctccccc tgtttgctta tgaatgcggg
8281 cgtgcccctc tctactgccc cccgttttcc gttcaggcta acgtggtttt ttcttcacca
8341 gcaccgagtg atcgtgacca cagtttcccg gatggcgaca cgcttctact tctacgcacg
8401 cagggcacag accgtgcccc tcaataacgt tatgtcgtag cgcaaaagccc attttagccg
8461 ccagcgtatg catgatgtct tccacgccc tccacacactc ttctttacc acgcccgaac
8521 gatcgagatg aaacatggcc gagctgtgcg tccgctggc gaacaggctgg caaacacat
8581 aactattggt ggattccact ttatggacaa aaccctgttc gagcaaaaaa tccagcgcg
8641 ggtaaatggt gggcgggttg gcctgtggtt ccgtttcgcg cagcaaatcg agcaaatcgt
8701 atgcgctgat ggcacccctgt tgcagactca tcaggcgag cacttcgagg cgctgaggcg
8761 tcaggcgcac gttgcgctgc gcgcagagtt ttccagcttg cgcagtaaac tcttgcgttg
8821 tggctctttt catgtagcac ctggaatggc atgaaagtct aatccgttac ttaccacga
8881 gctgcttaag actctgaat taccgcgca caatataatc cctgctaagc ttttcgcgc
8941 cagtattctc atctatacat aatgagggtc gatattataa caacaggatt taacatcact
9001 atttcacagc aatgattcgc ctctgtccgg taaagcggtg tggagggaatt acttcacctg
9061 ataataagat gggctaactg tgaacaaaaa cgtcaaatc tcactgatg ctatcgcggt
9121 ctgccttttt atggcaaaag aggcgagcgc gcccaatacc tggacggaag cgcgtaatga
9181 cgcaatgggc gggacgggag ttgcgtccgc gaattatggc agcggagtac tattaaatcc
9241 ggcgttactg gcaaaagcca aaccggaaga caatatacact gttgtccttc ctgcggtcgg
9301 cgtccagatt acggataaag acaatctcca ggaatgaatt gacgatatca gcgataaagt
9361 ggattactac gatgaggtcg tcgataacct tacgctgggg caaatctgc tcaatccgcg
9421 aggcgtgctg aatcaatttc agggcgccgc gcgcgacctg gccgatgagc tggaaatatt
9481 caacggaaaa accgcccgcg ccaatgccgc cgcggggttg gcgtaagta ttccagggca
9541 aacgcttttc gtggcggtta tcgcaaaagg ttaatgcgat gggcgcgta gttcgtccat
9601 tgaatcagaac gataatcagt atctgcgcga tatccagcat gatgaacgtg tccgcttcg
9661 tgaagcagga cgcgtgctt tgcgtgggtc tgacgaaatt acaagcatt taactctac
9721 cgcgtcgggg cgggtagcga ttgtatctga ctacggatatt gcgtggcga agcagtttgt
9781 ggtggcgag gtccctgttt ccatggcgt tacgccaaaa ctgcaaaaaa cctggctcta
9841 taactacacc acctcaattt ataactacga cagtagcgac tggaaatagca gccgttatcg
9901 caatgacgat acgggtttta acattgatgc gggccttgct gccgatatcg gtgaaaactg
9961 gacgctgggg gtgagcggac aaaaatctggt atctcgcat atcgatagca aagatattta
10021 catcactaat ggtatgacgg gagaaccac caactacaaa gatataacc aaatccgccc
10081 cctggttacc gcggcatcg catggcataa cgatttgctg accgtaagcg ccgatggcga
10141 tctgacggaa acgaaaggct ttaagagcga agacaattca cagtacgttg cgcctggcgc
10201 tgaagtctga cgttgtcat ggcctggcgt gcgcgaggg tatcgtcgg atgtgaaaaa
10261 taacgatagc aatgtggtta ccggcggtct tggcttgcg ccttttaacc gtgtgcatct
10321 cgatttaagt ggaactgacg gcgaagatga aacctggggg gcaggcgcg agcttacaat
10381 gacattctga ggtgctttca ccggaggcgc tacgctccg gtttagcgtt atgctatagt
10441 aacgccccct ttttaaccgg atgcttattt attcgccatg cagcctgaaa cccagtcctc
10501 cgctttacct gcttatcgct tctccatcgc gcctatgctc gactggacgg acagacattg
10561 ccgctatitc ctgcgtttgc tgcctgcca gacgcagctc tacaccgaaa tggtagccac
10621 gggcgcgatt attcacgcta agggtagcta tctggcttat agcgaagaag agcatccggt
10681 cgctctacag cttagtgtaa gcgatccggc tcagcttgcg catttgctaa agctggcgga
10741 agcgcgtggc tacgatgaaa ttaacctcaa cgtggggctc ccttccgac cgttgcaaaa
10801 cggatgtgtt ggcgcctgtt tgatgggcaa tgcgcaactg gtcccgatt gtgttaagc
10861 catgctgatg gtcgtctcga ttccggtagc ggtaaaaacc cgcattggtt ttgacgatca
10921 ggacagctat gcgtttctgt gtgatttcat cgatacggtt tccggtcagg gcgaatgcga
10981 gatgtttatt atccatgcgc gcaaagcctg gctttctggc ttaagccgga aagaaaatcg
11041 tgagatcccc ccgttggtt acccgcgcgt ctatcagcta aagcgggatt ttccgcacct
11101 gaccatgtcc attaacggcg gcatcaaatc gctggaagag gcgaaggagc acctgcgcca
11161 tatggatggc gtcatggttg gccgcgaagc ttatcagaat ccgggtatag tggcccggt
11221 ggatcgggag atttttgggc ccgataccac cgatgccgac ccggttgcgg tggttcgcg
11281 gatgtatccc tatattgagc gtaattgag ccaggagcgc tatctggggc atatcactcg
11341 ccataatgctg ggtttgttcc agggcatccc cggcgcgcg cagtggcgtc gctatctgag
11401 cgaaaacgcc cataaagctg gcgcggatgt tgcgtactg gagcaggcgc taaaactggt
11461 ggcagacaag cgttaaaagt tcgcaaaaaa ttagtcaatc tcaccacgcc ctgtgcagtc
11521 ttgcaggcgc ttttcttatt atatcaataa tataaatatt ggcatgattt ttgtaagggc
11581 ttacctgacc agaccggta agcgcggtgc gcgggggcaa tggcattttt atggggagcg
11641 actatgctgg aactactttt tgtgcttggc tttttctga ttttaattgt gacggcgctc
11701 tccctgctgg gcattctggc cgcgttggtt gtagcgactg ccgtcatgtt cctggcgga
11761 atgttcgccc tgatgatcaa gctgttaccg tggctactgc tggcggtggc tgtgtgtg
11821 gtgatcaag cagtaaaaac gccaaaaatc ccacagtatc agcgaataa ccgtcggttt
11881 tactaaggta ttgagcggtt cgtcacaacc tggaaacttg ccttcacag caaataggaa
11941 tcgattatta aatctgtcat gattgcgag gtaacgaatt catcgcgctg taccctacat
12001 acagccgaac aaaaaagaa agggcttccc ggggtggaagc ccaatttctt tgcagagcta
12061 ttacggaatc agcaggcttg agccctgtgt gggccggctt tccagcactt catgcgcgcg
12121 acgggcatct ttaacgcatt agcgttgatt ttcagccaca tcgactttaa tcacggcgct
12181 ggcgatcaat gagaacaatt cattgctggc ttcggtcagt tcttcagtg tcttaataa
12241 cccctgtagt gaaggctcgc tggcatagag ggaaccttfc tgattcagaa tacctaaatt
12301 cagccgggtg acggggccgg acgcattgcc gaaactgacc atcagtcgcc gacgttcag

12361 gcagtcacgt gaggcctccc aggtatcttt cccacaggag tcatagacca cgcggacttt
12421 ttggccgccc gtgattcttt ttaccggttc gacaatgtct tcttcacggg aattaattac
12481 ctgccaggca cggcgctcca gcgccgctg cgctttttgc gcgctaccga cgtaccgat
12541 aagcttcgcg cccagcgctt ttgccatttg gcaggcgatc agaccgacgc cggccgcagc
12601 ggcatgaaac aggaagggtt cgtcgggttt cacttcatag gttttgcgca acaggtaaaa
12661 aacgggtcaat cctttgagaa aagaggctgc cgcttgttcg aaagaaatgg cgtcaggcaa
12721 aatcgcggct ttatctcgcg tgacgttaig gacggaactg taagcgccga cgtttgactg
12781 cgcgtagacg acgcatcgc cgacgcgaat gtgctccacg cgtttgcgga ctttactgac
12841 cacaccgca gcttcgggtt ccaggcccgcc aggcacacgac gggggcggat agagtccgct
12901 acggatatag gtgtcgatga agttgatacc aatggctttg ttctcaacct ggatttcgtg
12961 ttccgcccgt tccgctggcg taaactccac ggtctgaagc acttccggac caccatgctt
13021 gtgaaattca atacgcgttg ccatgcttcc tccaaaagaa atgttgtaat ctttcgaccc
13081 aatcactatc tcggtaactc cattcactat ggcaggaaat aaaccttca acaaacaca
13141 gactgaigcc cgcgaccgcg atccgcagggt tgcggggata aaagtgcgcg cgcactcgat
13201 tgaagcggaa cagtcgggtt tggcggttt aatgctggat aacgagcgct gggacgatgt
13261 ggccgagcgc gtgttgcggg aagatttcta taccgcccgc catcgccata tctttacgga
13321 gatggggcgc ttgcaggaaa ggcgcagtc tctcgacctg attacgctcg cggaaatcgct
13381 ggagcggcag ggcacaactg acagcgtcgg cggtttcgcc tatctggcgg agctgtctaa
13441 aaacacgcca agcgcggcga atatcagtcg ttatgcggac attgtgcgcg aacgcggcgt
13501 ggtcccgcat atgatcgcg tggcgcatga aattgcggac gccggttacg atccacaggg
13561 gcgcaatagc gacgaactgc tggatctggc ggagtcgccc gtcctccaga tccgggaaaa
13621 ccgggccaac aaagacgaag gtccgaaaag catcgaccag atctcgacg ccaccgtggc
13681 gcgtatigag cagttgttcc agcaaccgca cgtatggcgtt acagcgctgg ataccgcta
13741 tcaggatctc aataaaaaa cggcagggtt acagcgttcg gatttgatta tctcgcggc
13801 gcgtccctcc atgggtaaaa ccacttttgc gatgaacctc tgcgaaaatg cggcgatgtt
13861 gcaagataag ccggtactga tctttagctt ggagatgccc ggcaacaga tcatgatcgc
13921 tatgtcggcc tcgctgtccc gcgtcgatca gacagctatt cgtaccgctc aacttgatga
13981 tgaagactgg gcgcgaatct ccggcacgat gggcattctg ctggagaaac gcaatatgta
14041 tattgacgac tcttcaggtc ttacgccgac agaagtcgct tccgcgcgcg ggcgtatttt
14101 ccgcgaacat ggccgggttaa gtctgattat gatcgactac ctgcaattga tgcgtgtgcc
14161 gtgcgtttct gataaccgtc ctctggaaat cgcggaaatt tctcgtcgtt tgaagcgct
14221 ggcgaaaggaa ctccagctga cgttcgtggc gctatcgag cttaccgctt ccttggaca
14281 acgcgcggat aaacgtccgg tgaactccga cctgcgtgaa tccggctcta ttgaacagga
14341 tgcggactta attatgttta tctaccgtga tgaggtttat caccgaaaca ggcacttaaa
14401 aggcattgct gaaattatta ttggtaaaga acgtaacggt cctatcggta cgttctgctt
14461 gacgttcaat ggtcagtggt cgcgttcga taactatgce ggaccgcaat acgatgatga
14521 gtaactctcc gtcaattctt taacaaggaa ttcaaatgca agcggcaaca gctgtcata
14581 accgcgcgcg tctgcgacac aacctgcaac gtctgcgtga actggcgctt gccagtaagc
14641 tggttgcggt ggtgaaagcg aacgcttatg gacacggctt tctggagacc ggcggaacgc
14701 tccctgatgc tgacgctttt ggcttggcgc gtcttgaaga ggctctacgt ctgcgagcgg
14761 cggggatcac gcagccaatc ctgctgctgg agggtttttt cgacgcgcgc gatttgcga
14821 ccatttccgc gcaatgtctg cataccgccc tacataatca agagcagctt gccgccctgg
14881 aggcgggtga gctggcggag ccggtaacgc tctggatgaa gctggatacc ggtatgcatc
14941 gtctcggcgt gcgtcccgaa gagcggaagg cgttctacca gcgtctgacg cactgtaaaa
15001 atgtacgcca gccggtgaat atcgtcagcc attttgcccg tgcggatgag ccggaatgce
15061 gcgtaccga acatcagctc gacattttta atgccttctg tcagggtaaa cccgtcagc
15121 gctctattgc cgcgtctggc ggtatcctgc tgtggccgca gcttcacttt gactggcgcc
15181 gtccggcgat cttttgtgat ggcgtatcgc cgttggagca caaaccttgg gggccggatt
15241 ttggttttca gccggtgatg tcttaacct ccagttgat cgcggtgctg gaccacaaag
15301 cggcgcaacc ggtggcctac ggcgggacat ggttgagtga gcgcgacacg ccttggcgcg
15361 tgggtggcat ggtttatggc gatggctacc cagcagcgcc gccctccggt acgccagtac
15421 tggtaaatgg tctgaaagt ccgattgtcg ggcgggtggc gatggatatg atttgcgtag
15481 atttggggcc aaacgcgcag gataacgcgg gcgatccggt ggtcttatgg ggtgaaggtc
15541 tgccggttga acgtatcgct gaaatgacaa aagtaagtgc ttacgaactt atcacgcgcc
15601 tgacctcaag ggtggcgatg aagtatattg attaaatagc cgcggcgccg gttggcgctt
15661 gcgcttatcc ggcctgtatc gcgcattggc tgtaggccgg ataagacgtt caccgcgtca
15721 tccgtaata tgcgcatcca ccacaacatc ctctcgatct tctcgtctt cgggtttatt
15781 gtgttatttc ctgcccctcg taaacctgga gaacctatgc gtgtttcaaa aagttagcgc
15841 ctatgccggc gatccgattc tticactgat ggagcggttt aaagacgact cccgtcacga
15901 caaagtgaat ctgagcattg gcctgtatga caacgaagac gggattatcc cacagcttaa
15961 aacggtggcc gaagccgaag cccggcttaa cgcgcagccg catggcgctt cgtgtacct
16021 gccgatggaa ggaactcaata ctatcgcca tactatcgcg cctttgtctt ttggcgccga
16081 tcaccgggtt ctacgacaac agcgcgtggc cactatccag acattaggcg gctccggcgc
16141 cgtgaaagta ggcgcggatt tcttgaagcg ttatttcccc gacgcagcgc tatgggtgag
16201 gcacccacc tgggaaaaac atattcgat atttgcgggg gcaggattcg aagttagtac
16261 ttacccttgg tatgacgacg cgactaacgg catccgtttt aacgatctgc tggccacgct
16321 gaatacggtt cctgcgcgca gtatcgtgtt gctgcacccc tgttgtcaca acccgaccgg
16381 ggccgattta acgcttctgc aatgggaigc ggtgattgaa atagtgaag cgcgcgatct
16441 gattccgttt ctgtatattg cctatcaggg gtttggcgca ggcagtgacg atgatcgta
16501 cgttatttgc gccatttgca gcgctgggtt acctgcgtta gtcagtaatt cttttcgaa
16561 gattttctcg ctgtacggcg agcgcgtcgg cggcctgtcc gtggtgtgtg aagatgctga

16621 aatcgccgcg cgggttctgg gacagctaaa agcgacggtg cgccgaattt actccagttc
16681 gccgtgtttc ggcgtcagg tggctgctac ggtcctgggc gatgaggcgt taaaagcggg
16741 ctggctggcg gaagtcgacg cgatgcgtaa ccgcattata tcatgccc agacgctggt
16801 gaaggagctg aaggcggaga tgcctgaccg caactttgat tacttgttac agcagcgcgg
16861 tatgttcagc tataccgggt taagcgagga gcaggtcgat cggttgcgcg atgagtttgg
16921 cgtttacctg attgccagtg gccgcattgt tgcgcgggg cttaatgctt caaatgtaca
16981 ccgcgtggcg aaggcatttg ccgctgtcat gtaatatca ggccggacgg cgataacagt
17041 gccctccggc ctgacaatag ctgttgtgat catcctcttt ttctgtaaca aaaccgcaga
17101 taatccttcc ttttgaccgt tactggcggt atggctcagat agtttttga gcaaagactc
17161 atcttaataa ttataatatt ttgaatttta agggaaaacc atgaaaaaaa taaccctggc
17221 gctgagtgcc gtctgtttgt tgtttacgct aaaccattcc gcgaatgcgt tagtatcttc
17281 cccttcgacg ctcaatccgg gcactaatgt tgcaaaactc gcggaacaag cgctgtcca
17341 ttgggtctct gtcgccaga ttgaaaacag cctcaccgga cgcccgccga tggcggtcgg
17401 ctttgatatt gacgacacgg tgttattttc cagccccgga ttctggcgcg gaaagaaaaa
17461 ctactccccg gacagcgacg attatctgaa aaatccggcc ttttgggaaa aaatgaacaa
17521 cggtgggatg gatttcagta ttccaaaaga agtggccgga cagctcattg atatgcatgt
17581 tcgccgtggc gacagtattt actttgtcac tggctgtagt cagacgaaaa cggaaaccgt
17641 gtcgaaaaac ctggcggaata acttccatat tccggcgccg aatatgaatc cggltgattt
17701 cgccgcgcat aaaccggaac aaaatcagaa agtacagtgg ctgcaggaga agaacaatgcg
17761 tatcttctac ggcgattcgg ataacgatat taccgcgccg cgtgatttgt gtatccggcg
17821 tattcgcatc ctgcgcggcg ctaactccac ctacaaaccg ctgcgcagg caggagcgtt
17881 tggcgaggaa gtcatgttca actcggagta ctaaaaatca ggagagcgac aggtctctct
17941 tttttgcatg atttttgcac aaacttgcgc cgtcggcttt taccttttcc agacttgtctg
18001 cacactattc aggagacgtt tgtttttagg aaggagcagc ctatgttgta tcagcgaccc
18061 attacacitga gcgagaagcc gcgcgggttt catctgataa cagatgaaat taccgataaa
18121 ttgtctggct taccgcctgt cgaacgggtt ttgctgcatc tttgttgtct acatfacctg
18181 gcctcgctga cgttaaacga aaactgcgat cccaccgtgc gcgctgatat ggagcgccat
18241 ttctgaaaaa ccgttcccga taatgcggcg tatgaacatg attacgaagg cgcgatgac
18301 atgccttcgc atattaagtc gtcagttatt ggctgtctgt tgcgtcgtcc tgtacggcag
18361 gggcgtttac agttaggaac atggcaaggt atctgttgg gagagcaccg tattcacggc
18421 ggtccacgta aaatcatcgc gacactacaa ggggaatgat aatgaccatt tcggaattac
18481 tgcaatactg catggcaaaa cctggcgag agcagagcgt ccacagcgac tggaaaagcga
18541 cgcaaatlaa agtgaagat gtacttttcg cgttggtaaa agaagtgaag ggacgcccgc
18601 cagcctctct caaaaccagc ccggaactgg cagagtgtt acgtcagcag cacagcgatg
18661 tacgaccgag tcggcacctt aataaagcgc actggagcac ggtctatctg gacgctcgc
18721 tgccggattc acaactctat tatctggtcg atgctctta tcaacaggcg gtaaatgcgc
18781 tgcggaaga taaacgcaag cagttgccc agtcttgatt atagcgccc gaccaacaac
18841 gccagggcga tatcaatgag gcggatgacc gttagaccga tacgcttgcg gaggggcatt
18901 tgcgcatatt tggcgcgtag cctggcgagg tcccgtgtc ctccagcag aataatcata
18961 tgcgtcgtct ccagccagcc gcgagcatgt tctgaagcg ccgcccgat aaaccgcccg
19021 gactcgcgga tagcgtcgtc gctgtcttct ctgtcctgtc tatagctcg gataaactcg
19081 gcaatcgccg aggacgctac aggtgttgc gcctggcgcg tegtatcag gtaattgtat
19141 tcgttaatag acgcaatttt catctccctg agtgcagcgg cgcccccatt cgagacactc
19201 gccctgtatg gctaatttcc agacctgatt attttgcgt tegtatctct cagcctggat
19261 gtaagttaagt ggttgcctac gtcgcataac ccgcgcataa agacgcaaat agtgattttt
19321 cagcagcgcc agattatcga gacgggtgtt atccccacct tgacggcgga cccgctcagc
19381 ctgaaaaaat atctggcgga tatcgcggtc atccttgagc agtgcctctt ttgtccacgg
19441 taticgcgcc gcgtcttga ggaagcgggt tgagcgcgct tglaatagcg ttagttgttg
19501 aaaagccagc gcgttaaagc ggtcaggcag cgtacaggcg gataaaaaa ggcacagcag
19561 tagtgtgatt gcgtaggcca acttcattgt gtttccata acagaccgtt tgcgctatca
19621 catgtcagag cgaggcgcca cgcaaatcac aaatgctcaa cacggatata atgaggtggg
19681 atgaggaaaa atgatgccgc ttcccgcgga atcggaagc ggcgtgaagg ttatttgagc
19741 ataggtttaa ggaagcggcg ggtatgcgac gcctcgcaat ccgccacggt ttccggcgta
19801 ccggcgacga gaatttcgcc gccgcgctg ccgccttccg ggcggaggtc gacaatccag
19861 tccgccgttt taatgacgtc caggttgtgt tcatcacca cgttggtgtt gccctgatcg
19921 cgcaactgat gcagaacgtc aagcaactgc tgaatatcgg caaagtgcag gccgttggtt
19981 ggctcgtcga gaatatagc cgtctgcccg gtgcgcgtc tcgacagttc gcgcggcagc
20041 ttacgcgctt gggcctcgcc gccggaaaag gtgtgcggc actgaccaag acggatatag
20101 gtcagcccta cgtccatcag cgtctgcagc ttacgcgcca gccccggaac cgcatacaag
20161 aactcacgcg ctcttctaag ggtcatatcc agcacttctg ggttggtctt gcccttgtac
20221 ttaatttcca gcgtttccc gttatagcgc ttgcctttgc actggtcgca cggcacgtaa
20281 atatccggca gaaagtgcgt ttgcacttta atgacgcat cgccctggca cgttctcag
20341 cgaccgcccgc gcacgttgaa gctgaatcgc cctggcggtt agccgcgcca gcgagactcc
20401 ggcacggcag caaaaagctc gcgaaccggg gtaaaagacg ccgtataggt cggcggttg
20461 gaacgcgggg tgcgccgat tggcctcgtg tcgatatcga tcactttatc gaaatgttcc
20521 agccctgaa tatcccgata cggcgccggt tcggcgatag tgcgccgtt taactgacgc
20581 tggcgatgg ggaacagcgt gtcgttaatc agcgtcgatt taccggaacc cgagacggcg
20641 gtgatacagg taaacagccc taccggtagc gtaagggtca catctttcag gttgttgcgc
20701 cgcgcggcgg tgagtttagc cacttttctt ggaatttgcg gcacgcgttt ttccggcact
20761 tcaattttgc gtttaccgct catgtactgg ccggtcagcg attccggtag cgccataatg
20821 gcttccagcg gcccttccgc caccacctcg ccgctgtaa cgcccgccc gggcccaata

20881 tcaatcacat ggtcggcggc gcaaatggcg tcttcatcgt gtccaccac aatcacggta
20941 ttgccaaagt tgcgcagatg aatcagcgt cccagcagcc gtctgttata gcgctgggct
21001 agaccgatgg acggctcctc cagcacatac atcacgccga ctaacccggc gcctatctgg
21061 ctgcgcagac gaatacgtcg ggcttcgccc cgggaaagcg tctctgccga gcgggagagc
21121 gtgagatagt tcaggccgac gtccaccaga aacttgaggc gatcgccgat ctcttttagc
21181 actttttcgg cgattttcgc tctgtgccc gaaagcttga gattagttaa aaaatccatc
21241 gcatggccaa tgcctcatatc agaaatagca ggagcggcg tattttccac aaatacatgg
21301 cgcgcttcgc gattcagtcg cgtgccctca cagctggcgc agggcgatt actgatgaac
21361 ttgcgcagct cttcgcgcac cgcgctggat tccgtctctt tataacggcg ctccatatta
21421 tgcagcacgc cttcgaacgg atggcggcgc acggaggat cggcgcatc gtccatata
21481 ttaaattcaa tgttctctt gccggaaccg tacagcacga ctattgtac gtggcgctg
21541 aggcttgccc acggcgcatc tacgtcgaa ttatagtgtt ccgccagcga cttagcatt
21601 tgaaagtagt aaaaattgcg acgatcccaa ccacgaatcg cggcgctgc cagcgacagg
21661 tcgggattct ggcacacgc gtccggatcg aaatatgtt gaacggcag gccgtcacag
21721 gtccggcagg cgcttcggg gtgttgtaac gagaacagac gcggttcag ctgcgcata
21781 ctgtagccgc aaatcggaca ggcaaaatg gcggagaaca gaagctctc cgtttctca
21841 tctccatat cggaacaac cgcgctgcgc cgggataatt ccagccgctt ttcgaacgac
21901 tccgccaggc gttgggaaag atcgttcgca actttgaagc gatcgatcac cacctcaatg
21961 gtatgtttct ttgtagctc cagcttcggc ggcacggaga gatcgagac ttccgctca
22021 atacggcgcc gaattgaacc ctggcttgcc agattttcca gcgttttgt gtgttcgct
22081 ttacgctctt taataatcgg cgcgagcagc atcagacgtt tgccttcgg ctgtgacagc
22141 acgttatcga ccatctggct aacggtttgc gccgccagcg gcagctatg atccggacaa
22201 cgcgcttcgc ccacgcggcg aaacagcagg cgcaggtagt cgtggatctc ggtaatagta
22261 cccaccgtag agcgcgggtt gtgcgatgtc gatttctgtt caattgagat cgcggcgat
22321 agccctcaa tatggctgac atccggtttt tccatgagcg acaaaaatc cgcgcgtaa
22381 gcggagagcg attcaacgta acgacgtgc ccttcggcat acagagtgct gaaagccagt
22441 gaggatttgc ctgaaccgga aagcccggtc acgacaatca gttgtcgcg ggggatgacg
22501 aggttaatat tttgagatt atgggtgcgg gcgccccgaa cttcgatctt atccattcac
22561 ctttccgggt agagactcgg atgcctggtt ttttgaagg acaaacggca gaaacggcta
22621 attatgacac aatttaacct gtitgaatat acagtattgg aatgcactt cagctaaagt
22681 atgcaacaat atgaggttgc cgcgagtgac ctggaacctg catcgagct attaaaatgc
22741 tacgtggaaa tggtaacatc acgcgtttac actatttatg aaacgtattc aggagactca
22801 attatggcca gcagaggcgt aaacaaggta attctcgttg gtaatctggg ccaggacccg
22861 gaagtacgct atatgccgag tggcggcgct gtccccaact taacgctggc tacttctgaa
22921 tccgtggcgcg ataagcagac cggcgaaatg aaagagcaga ctgaatggca cgggtgtgtg
22981 atgttcggca aactggcggg agtggccggc gaatatctgc gtaagggttc tcagggttat
23041 atcgaaggtc aattgcgtac ccgcaagtgg accgatcaga gtggccagga acgctatagc
23101 actgaaatta acgttcgca gatcggcggc gtgatgcaga tgcgtgggtg tccaggggc
23161 ggccgcgcac cggcagcggc tcagcagcag gggggttggg gtccagccga acaacctcag
23221 cagccgcagg gcggcaacca gticagcggc ggcgcgcagt cgcgtccaca gcaatcccg
23281 ccagccgggt ctaacgaacc gccaatggat tttagcagc acattccgtt ctgatttttg
23341 gtaaaaaact caaagcgta ttgtcatctt cgtatagtt ctgctcgtt gaaatgcctg
23401 gtgtaacca ggcatcttct tacctggat tatgtcttt gtatccctt caaaaagag
23461 aagcgcatat cttagcgaaa aatgtcgtt atgcctctg gccgactcgc ctccggcacat
23521 cattatccag ccgaagttca taaatgtact gcaataaccg ggaattgtctt aaatatgaaa
23581 gagaaatctc atctgcaaaa tatataatgt atagccattt tttagacaaca aaaagatatt
23641 ataaaaaac ggtagagaa gticgggtatt atcaatggtt aattaaatgt ttgttttagc
23701 ttgtgatgag ctcaaatatg atatgtgtat ctgtctttt ttttaattgc tgaagataaa
23761 attgttactt atagctggct ttataaaaa aatgggttta ttgtgtatt ttttacaca
23821 attctgattt ttactcccc acttattata tttcaatga ttaagtatt attgaagtcc

//

SRS 6.1.3.11 | [feedback](#)